

RESULT 2
ID 091988 PRELIMINARY: PRT: 286 AA.
AC 091988;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE NEUROPHILIN-6 PRECURSOR.
OS Xiphophorus maculatus (Southern platyfish), and Xiphophorus helleri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Acanthopterygii;
OC Atherinomorpha; Cyprinodontiformes; Cyprinodontidae; Poeciliidae;
OC Xiphophorus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95039452.
RA Goltz R., Koster R., Winkler C., Raulf F., Lottspeich F., Scharlt M.,
RA Thoenen H.;
RT "Neurophilin-6 is a new member of the nerve growth factor family.";
T Nature 372:266-269(1994).
EMBL; L36942; AAA61923.1; -
EMBL; L36323; AAA61922.1; -
EMBL; L36326; AAA61921.1; -
DR HSSP; P01139; 1BTG.
DR INTERPRO; IPRO02072; -
DR PFAM; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PROSITE; PS00248; NGF; 1.
DR PRODOM; PD002052; -; 1.
KW Signal.
FT CHAIN 1 142 NEUROPHILIN-6.
SQ SEQUENCE 286 AA; 31424 MW; 5607DBA66792E12D CRC64;

Query Match 58.7%; Score 429; DB 13; Length 286;
Best Local Similarity 63.0%; Pred. No. 8.2e-39;
Matches 85; Conservative 11; Mismatches 27; Indels 12; Gaps 4;

QY 6 LHRREYSCDSEHWGVLQATDLRGNEVYLPVIRINNVYKKOMFEYETTCRVSKP--- 62
DB 149 MHRREYSCDSEHWGVLQATDLRGNEVYLPVIRINNVYKKOMFEYETTCRVSKP 205
QY 63 -----IGAPKRGQ-GVSGKAGTSCRGIDNEHNSYCTNHTFVALTSYKQIAMRFIRI 116
DB 206 SSGIYIGRSGRGKSGKSGTSGNSCGRIDSKRYMNSHCINTDIYASLTVEKQIAMRFI 265
117 RINACVCLSRNSW 131
266 RINACVCLSRNSW 280

RESULT 3
ID 090KL8 PRELIMINARY: PRT: 241 AA.
AC 090KL8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE NERVE GROWTH FACTOR B.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99256269.
RA Tong Y., Wang H., Chen W.;
RT "Cloning and sequencing of the gene for premature beta nerve growth
factor.";
RL Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).
RN [2]

RP SEQUENCE FROM N.A.
RA Tong Y., Wang H.;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF150960; AAD55975.1; -
DR INTERPRO; IPRO02072; -
DR PFAM; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PROSITE; PS00248; NGF; 1.
SQ SEQUENCE 241 AA; 26959 MW; 619DFC65EB3BD671 CRC64;

Query Match 50.4%; Score 368.5; DB 4; Length 241;
Best Local Similarity 54.2%; Pred. No. 2.5e-32;
Matches 71; Conservative 13; Mismatches 32; Indels 15; Gaps 1;

QY 2 ANDLHREYSCDSEHWGVLQATDLRGNEVYLPVIRINNVYKKOMFEYETTCRVSK 61
DB 124 SHDIFHRGERSVCDVSVMWGDKTTATDIKGEVMVLGEVINNSVFKOYFEETKCDPN 183
QY 62 PIAPKPGCGVSGVAKTSCRGIDNEHNSYCTNHTFVALTSYKQIAMRFIRINAA 121
DB 184 PV-----DSCRGIDSKRMSYCTTHTFVALTMDGQAMRFIRIDTA 228
QY 122 CVCVLSRNSWR 132
DB 229 CVCVLSRKAIR 239

RESULT 4
ID 097TC3 PRELIMINARY: PRT: 87 AA.
AC 097TC3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE BETA NERVE GROWTH FACTOR (FRAGMENT).
GN NGF.
OS Cervus elaphus scoticus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA Robertson T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
RA Suttie J.M.;
RT "NGF expression in Antler.";
RT Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF145043; AAF17235.1; -
DR INTERPRO; IPRO02072; -
DR PFAM; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
FT NON_TER 1
FT 87 87
SQ SEQUENCE 87 AA; 9876 MW; 17E06E49AFA7A0A4 CRC64;

Query Match 35.8%; Score 261.5; DB 6; Length 87;
Best Local Similarity 52.0%; Pred. No. 3.1e-21;
Matches 51; Conservative 7; Mismatches 25; Indels 15; Gaps 1;

QY 20 WGNLQATDLRGNEVYLPVIRINNVYKKOMFEYETTCRVSKDIGAPKPGVSGVAGT 79
DB 5 WGDGKTATDIKGEVMVLGEVINNSVFKOYFEETKCDPN-----D 49
QY 80 SSCRGIDNEHNSYCTNHTFVALTSYKQIAMRFIR 117
DB 50 GCGRGIDAKHNSYCTTHTFVALTMDGQAMRFIR 87

RESULT 5
ID 097759 PRELIMINARY: PRT: 247 AA.

AC 097759;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE BRAIN DERIVED NEUROTROPHIC FACTOR.
 GN BDNF.
 OS Allurus fulgens (lesser panda).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Feng L.;
 RT "Giant Panda (GP) and Lesser Panda (LP) BDNF gene sequences and their
 deduced amino acid sequences.";
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U56639; AAD10843.1; -
 DR HSSP; P23560; 1B8M.
 DR INTERPRO; IPR002072; -
 DR PFAM; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR PROSITE; PS00248; NGF; 1.
 DR PRODOM; PD002052; -; 1.
 SQ SEQUENCE 247 AA; 27870 MW; FE8C62CF1A6C03EE CRC64;

Query Match 35.4%; Score 259; DB 6; Length 247;
 Best Local Similarity 44.5%; Pred. No. 1.9e-20;
 Matches 57; Conservative 12; Mismatches 41; Indels 18; Gaps 4;

QY 3 NDLHGEYVCDSEEHV--GNLTQATDLGNEVTYLPVRINNVKQMEYETTCVSV 60
 DB 130 SDAKRGELSYCSISIMVYAAADKKTAVDMSGGVTVLEKTPVKGQAKQFYERK--- 186
 QY 61 KPIGAPKPGGSGVAGTSSCRGIDNEHNSYCTNVHTFVRLT-SYKNOIAMFEIRIN 119
 DB 187 NPGYTKREG-----CRGIDKRHNMSQCRTOQSYRALTMDSKRRIGWFRIRID 234
 QY 120 AACVCYL 127
 DB 235 TSCVCTLT 242

RESULT 6
 ID 09YH42 PRELIMINARY; PRT; 270 AA.
 AC 09YH42;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE BRAIN DERIVED NEUROTROPHIC FACTOR.
 GN Brachydanio rerio (zebrafish) (zebra danio).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hashimoto M., Heinrich G.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42489; AAD00016.1; -
 DR HSSP; P23560; 1B8M.
 DR INTERPRO; IPR002072; -
 DR PFAM; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR PROSITE; PS00248; NGF; 1.
 DR PRODOM; PD002052; -; 1.
 SQ SEQUENCE 270 AA; 29482 MW; 6BF136101B4E45C0 CRC64;

Query Match 34.1%; Score 249; DB 13; Length 270;
 Best Local Similarity 45.1%; Pred. No. 2.6e-19;
 Matches 55; Conservative 12; Mismatches 37; Indels 18; Gaps 4;

QY 9 GEYSVCDSEEHVGNLTQAT--DLGNEVTYLPVRINNVKQMEYETTCVSVKPIGAP 66

DB 159 GELSVCDSEEHVGNLTQAT--DLGNEVTYLPVRINNVKQMEYETTCVSVKPIGAP 215
 QY 67 KPGQGVSVKAGTSSCRGIDNEHNSYCTNVHTFVRLT-SYKNOIAMFEIRINACVY 125
 DB 216 KEG-----CRGIDKRHNMSQCRTOQSYRALTMDSKRRIGWFRIRIDTSCVCT 263
 QY 126 LS 127
 DB 264 LT 265

RESULT 7
 ID 09YX95 PRELIMINARY; PRT; 324 AA.
 AC 09YX95;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE NEUROTROPHIN PRECURSOR.
 GN NTL.
 OS Lampetra fluviatilis (River lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE; 99003404.
 RA Hallbook F., Lundin L.G., Kullander K.;
 RT "Lampetra fluviatilis neurotrophin homolog, descendant of a
 RT neurotrophin ancestor, discloses the early molecular evolution of
 RT neurotrophins in the vertebrate subphylum.";
 RL J. Neurosci. 18:8700-8711(1998).
 DR EMBL; AF071432; AAD22744.1; -
 DR INTERPRO; IPR002072; -
 DR PFAM; PF00243; NGF; 1.
 DR CHAIN 141 324
 FT CHAIN 141 324
 SQ SEQUENCE 324 AA; 35267 MW; 9D6B56C1978F8485 CRC64;

Query Match 33.4%; Score 244.5; DB 5; Length 324;
 Best Local Similarity 37.6%; Pred. No. 9.7e-19;
 Matches 56; Conservative 16; Mismatches 46; Indels 31; Gaps 5;

QY 7 HRGEYVCDSEEHVGNLTQATDLGNEVTYLPVRINNVKQMEYETTCVSVKPIGAP 49
 DB 175 HRGEYVCDSEEHVGNLTQATDLGNEVTYLPVRINNVKQMEYETTCVSVKPIGAP 234
 QY 50 QMEYETTCVSVKPIGAP-----KPGQGVSVKAGTSSCRGIDNEHNSYCTNVHTF 100
 DB 235 QFYERK---KPAAGAGTGRSRAFSAGTGTG-SACGADBLFRSCKTOSF 290
 QY 101 VRLT-SYKNOIAMFEIRINACVYLSR 128
 DB 291 VRLTSDARGRLAMRWIRLDTACVCTLR 319

RESULT 8
 ID 09TT22 PRELIMINARY; PRT; 101 AA.
 AC 09TT22;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).
 GN BDNF.
 OS Macaca fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;

RA Hashimoto T., Okuno H., Tokuyama W., Li Y.-X., Miyashita Y.?
RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
RT their receptor messenger RNAs in monkey rhinal cortex.";
RL Neuroscience 0:0-0(1999).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE: 99270338.
RA Okuno H., Tokuyama W., Li Y.-X., Hashimoto T., Miyashita Y.?
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathw
RT in adult macaque monkeys.";
RL J. Comp. Neurol. 408:378-398(1999).
DR EMBL: AF208982; AAF24762.1; -.
DR INTERPRO: IPR002072; -.
DR PFEAM: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR PROSITE: PS00248; NGF; 1.
FT NON_TER 1
FT NON_TER 101
FT NON_TER 101
SEQUENCE 101 AA; 11476 MW; D6A56BD497961740 CRC64;

Query Match	31.2%;	Score 228;	DB 6;	Length 101;
Best Local Similarity	44.3%;	Pred. No. 1.6e-17;		
Matches	51;	Conservative	10;	Mismatches 36;
			Indels	18;
			Gaps	4

[illegible]

RESULT	9			
002790				
ID	002790	PRELIMINARY;	PRT;	85 AA.
AC	002790;			
DT	01-JUL-1997 (TREMBLrel. 04, Created)			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DE	BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).			
GN	BDNF.			
OS	Macropus fuliginosus (Western gray kangaroo).			
OC	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.			
	[1]			
	SEQUENCE FROM N.A.			
RL	Kullander K., Carlson B., Hallbook F.;			
RL	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; U93381; AAB58686.1; -.			
DR	HSSP; P23560; IBBM.			
DR	INTERPRO; IPR002072; -.			
DR	PEAM; PFE00243; NGF; 1.			
DR	PROSITE; PS00248; NGF; 1.			
FT	NON_TER	1	85	1
FT	NON_TER	85		
SQ	SEQUENCE	85 AA;	9618 MW;	E42189F012AB1ED CRC64;

Query Match	22.0%;	Score 160.5;	DB 6;	Length 85;
Best Local Similarity	42.2%;	Pred. No. 2.8e-10;		
Matches	38;	Conservative	6;	Mismatches 31;
			Indels	15; Gaps 2

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QY 16 SEEHVGNLTQATDILRGNEVATLPHVIRINNNYKKMEYETTERSKPTAPAPPGQGVSV 75
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 3 SEWTVGGRKTRAVDMSCGVTVLEKVPVPGKQKQYETKC---NPMGYTRKG----- 53
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 76 KAGTSSCGIDNEHNNSYCTNHTVTRALT 105
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 54 -----CRGIDRRHNNSSQRTQSYVTRALT 77
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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RESULT	10			
042312				
ID	042312	PRELIMINARY;	PRT;	42 AA.
AC	042312;			
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)		
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)		
DE	NERVE GROWTH FACTOR (FRAGMENT).			
GN				
OS	Cyprinus carpio. (Common carp).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;			
OC	Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kullander K.;			
RA	J. Mol. Evol. 45:0-0(0).			
RF	[2]			
RA	SEQUENCE FROM N.A.			
RA	Hallbook F., der Lehr N.;			
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF008557; AAB63508.1; -			
DR	HSSP; P01139; 187G.			
DR	INTERPRO; IPR02072; -			
DR	PFAM; PF00243; NGF; 1.			
FT	NON_TER	1		
FT	NON_TER	42		
FT	NON_TER	42		
CO	SEQUENCE	42 AA;	4649 MW;	41B72D1BF67F742 CRC64;

Query Match	21.5%;	Score 157.5;	DB 13;	Length 42;
Best Local Similarity	49.1%;	Pred. No. 2.6e-10;		
Matches 28; Conservative	8;	Mismatches 6;	Indels 15;	Gaps 1.

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0Y      56  TCORVSKPFGACRKPQGVGVSAGTSSCGCIDNEHNSYCTVHFFVRLATSYKNQIA 112
      ||| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
Db      1  TCR-----GPRTGSSGCLGIDSRHNSICTNTHTYVRLATSFEDQVA 42

RESULT  11
002792
ID      002792      PRELIMINARY;      PRT;      85 AA.
AC      002792;
DT      01-JUL-1997 (TrEMBLrel. 04, Created)
DT      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT      01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE      BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).
GN      BDNF.
OS      Notoryctes typhlops (Marsupial mole).
OC      Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Metatheria; Notoryctemorphia; Notoryctidae; Notoryctes.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kullander K., Carlson B., Hallbook F.;
RL      Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U93380; AAB56685.1; -.
DR      HSP; P23560; 188M.
DR      INTERPRO: IPR002072; -.
DR      PRAM; PF00243; NGF; 1.
DR      PROSITE; PS00248; NGF; 1.
FT      NON_TER      1      85
FT      NON_TER      1      85
SQ      SEQUENCE      85 AA;      9577 MW;      33754EPA015314661 CRC64;

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RESULT	11
ID	002792
AC	002792;
DT	01-JUL-1997 (TrEMBLrel. 04, Created)
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE	BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).
GN	BDNF.
OS	Neurocytes typhlops (Marsupial mole).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Mammalia; Notoryctemorphia; Notoryctidae; Notoryctes
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Kullander K., Carlson B., Hallbook F.;
RL	Submitted (MAR-1997) to the EMBL/Genbank/DDB databases.
DR	EMBL; U03380; AAB58685.1; .
DR	HSSP; P23360; I38M.
DR	INTERPRO; IPRO02072; .
DR	Pfam; PF00243; NGF; 1.
DR	ProSITE; PS00248; NGF; 1.
FT	NON_TER
FT	NON_TER
SO	SEQUENCE
	85 AA; 9577 MW; 33754EA01531A661 CRC64;

Query Match	21.1%	Score 154.5	DB 6	Length 85
Best Local Similarity	40.2%	Pred. No. 1.2e-09		
Matches 37	Conservative 6	Mismatches 32	Indels 17	Gaps 3

QY 16 SEEHV--GNLTQATDLRGNEVTVLPHVRINNVKKQMEYETTCRVSKPIGAPXPGQGS 73

Db 1 SISEWTAADKTAIVDMSGTIVLEKVPYKPKGOLKQYFETKC---NPMGYTKEG----- 53

OY 74 GYKAGTSSCGIDNEHNSYCTNVHTFVRALT 105

Db 54 -----CRGIDKRHMNSOCRTQSYVRALT 77

RESULT 12

ID 002795

AC 002795

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).

GN BDNF.

OS Ornithorhynchus anatinus (Duckbill platypus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.

[1]

SEQUENCE FROM N.A.

RA Kullander K., Carlson B., Hallbook F.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

EMBL: U93376; AAB58681.1; -.

DR HSSP: P23560; 188M.

DR INTERPRO: IPR002072; -.

PFAM: PF00243; NGF; 1.

DR PROSITE: PS00248; NGF; 1.

FT NON_TER 1

FT NON_TER 85

SO SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match

Best Local Similarity 21.1%; Score 154.5; DB 6; Length 85;

Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

OY 16 SEEHV--GNLTQATDLRGNEVTLPHVRINNYYKKMFETTCRVSKPIGAPKPGQGV 73

Db 1 SISEWTAADKTAIVDMSGTIVLEKVPYKPKGOLKQYFETKC---NPMGYTKEG----- 53

OY 74 GYKAGTSSCGIDNEHNSYCTNVHTFVRALT 105

Db 54 -----CRGIDKRHMNSOCRTQSYVRALT 77

RESULT 13

ID 002798

AC 002798

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).

GN BDNF.

OS Petrusus breviceps (Australian sugar glider).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Metatheria; Diprotodontia; Petauridae; Petaurus.

[1]

SEQUENCE FROM N.A.

RA Kullander K., Carlson B., Hallbook F.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

EMBL: U93377; AAB58682.1; -.

DR HSSP: P23560; 188M.

DR INTERPRO: IPR002072; -.

PFAM: PF00243; NGF; 1.

DR PROSITE: PS00248; NGF; 1.

FT NON_TER 1

FT NON_TER 85

SO SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match

Best Local Similarity 21.1%; Score 154.5; DB 6; Length 85;

Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

OY 16 SEEHV--GNLTQATDLRGNEVTLPHVRINNYYKKMFETTCRVSKPIGAPKPGQGV 73

Db 1 SISEWTAADKTAIVDMSGTIVLEKVPYKPKGOLKQYFETKC---NPMGYTKEG----- 53

OY 74 GYKAGTSSCGIDNEHNSYCTNVHTFVRALT 105

Db 54 -----CRGIDKRHMNSOCRTQSYVRALT 77

RESULT 15

ID 013104

AC 013104

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).

GN BDNF.

OS Cercartetus laudus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Metatheria; Diprotodontia; Burramyidae; Cercartetus.

Best Local Similarity 40.2%; Pred. No. 1.2e-09; Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

OY 16 SEEHV--GNLTQATDLRGNEVTLPHVRINNYYKKMFETTCRVSKPIGAPKPGQGV 73

Db 1 SISEWTAADKTAIVDMSGTIVLEKVPYKPKGOLKQYFETKC---NPMGYTKEG----- 53

OY 74 GYKAGTSSCGIDNEHNSYCTNVHTFVRALT 105

Db 54 -----CRGIDKRHMNSOCRTQSYVRALT 77

RESULT 14

ID 002801

AC 002801

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).

GN BDNF.

OS Tachyglossus aculeatus (Australian echidna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Monotremata; Tachyglossidae; Tachyglossus.

[1]

SEQUENCE FROM N.A.

RA Kullander K., Carlson B., Hallbook F.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

EMBL: U93383; AAB58681.1; -.

DR HSSP: P23560; 188M.

DR INTERPRO: IPR002072; -.

PFAM: PF00243; NGF; 1.

DR PROSITE: PS00248; NGF; 1.

FT NON_TER 1

FT NON_TER 85

SO SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match

Best Local Similarity 40.2%; Pred. No. 1.2e-09; Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

OY 16 SEEHV--GNLTQATDLRGNEVTLPHVRINNYYKKMFETTCRVSKPIGAPKPGQGV 73

Db 1 SISEWTAADKTAIVDMSGTIVLEKVPYKPKGOLKQYFETKC---NPMGYTKEG----- 53

OY 74 GYKAGTSSCGIDNEHNSYCTNVHTFVRALT 105

Db 54 -----CRGIDKRHMNSOCRTQSYVRALT 77

Mon Oct 30 10:20:10 2000

us-09-157-984-1.rsp

Page 6

FT	NON_TER	85	85
SQ	SEQUENCE	85 AA;	9604 MW; 33754EA01520B661 CRC64;

Query Match	21.1%	Score 154.5	DB 6	length 85
Best Local Similarity	40.2%	Pred No. 1.2e-09		
Matches 37; Conservative	6	Mismatches 32	Indels 17	Gaps 3

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QY 16 SEEHV--GNTLQADIDKNGNETVTPHRRINNVKKOMEYETTCVSKRIGAPKRGQGS 73
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 SISEWVTAADKRTAIDMSGGTYTVLEKTPVPRGQGLQYFYELK---NPMGTKEG----- 53
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 74 GVKAGTSSCRGIDNEHNSYSCYNVHTEPRALF 105
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 54 -----CRGIDKRHHNSQCKTQISYVRAFL 77
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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Search completed: October 28, 2000, 12:38:30
Job time: 9819 sec